

Structure of Bacteriorhodopsin at 1.55 Angstrom Resolution

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The atomic structure of the light-driven ion pump bacteriorhodopsin and the surrounding lipid matrix was determined by x-ray diffraction of crystals grown in cubic lipid phase. In the extracellular region an extensive 3-dimensional hydrogen-bonded network of protein residues and seven water molecules leads from the buried retinal Schiff base and the proton acceptor Asp 85 to the membrane surface. Near Lys 216 where the retinal binds, transmembrane helix G contains a π -bulge that causes a non-proline kink. The bulge is stabilized by hydrogen-bonding of the main-chain carbonyl groups of Ala 215 and Lys 216 with two buried water molecules located between the Schiff base and the proton donor Asp 96 in the cytoplasmic region. The results indicate extensive involvement of bound water molecules in both the structure and the function of this seven-helical membrane protein. A bilayer of 18 tightly bound lipid chains forms an annulus around the protein in the crystal. Contacts between the trimers in the membrane plane are mediated almost exclusively by lipids.

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